

SEQUENCE LISTING

<110> DYAX Corp.
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Luneau, Christopher J.
Ladner, Robert C

<120> NOVEL ENTEROKINASE CLEAVAGE SEQUENCES

<130> DYX-012.1 US, DYX-012.1 PCT

<140> not yet assigned
<141> 2001-06-19

<150> US 09/597,321
<151> 2000-06-19

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<170> PatentIn version 3.1

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30

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<211> 7

<212> PRT

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<400> 147

Pro His Ile Glu Asp Arg Met
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<210> 148

<211> 7

<212> PRT

<213> synthetic enterokinase cleavage sequence

<400> 148

Ser Gly Gly Asp Asp Arg His
1 5

<210> 149

<211> 7

<212> PRT

<213> synthetic enterokinase cleavage sequence

DRAFTED * APPROVED * RELEASED

<400> 149

Glu Val Phe Ala Asp Arg Ser
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<210> 150

<211> 7

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<400> 150

Gly Leu Ala Glu Asp Arg Thr
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<210> 151

<211> 7

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<400> 151

Ser Gly Gly Asp Asp Arg Leu
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<210> 152

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<400> 152

Ser Gly Gly Asp Asp Arg Met
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<211> 7

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<400> 153

Gly Leu Val Ser Glu Arg Gly

03834794701601

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<400> 154

Gly Gly Phe Glu Asp Lys Met
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<210> 155
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<400> 155

Ser Leu Asp Asp Asp Arg Thr
1 5

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<400> 156

Asp Val Tyr Ser Glu Arg Met
1 5

<210> 157
<211> 7
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<400> 157

Asn Met Asp Trp Asp Arg Ser
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DRAFT - NOT FOR RELEASE

<210> 158
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<400> 158

Ser Leu Asp Asp Asp Arg Thr
1 5

<210> 159
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Gly Ser Gly Gly Asp Arg Met
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Phe Ser Glu Glu Asp Arg Met
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<400> 161

Ser Leu Asp Asp Asp Arg Thr
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<213> synthetic enterokinase cleavage sequence

<400> 162

Val Asp Met His Asp Arg Met

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<210> 163

<211> 7

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<400> 163

Ser Gly Gly Asp Asp Arg Met

1 5

<210> 164

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<212> PRT

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<400> 164

Asn Val Arg Met Asp Arg Ser

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<210> 165

<211> 7

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<400> 165

Ser His Arg Asp Glu Lys Val

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<211> 7

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<400> 166

Leu Met Asn Asp Asp Arg Ala
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Phe Val Met Asn Asp Lys Gly
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Gly His Val Asp Asp Arg Met
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His Ala Ile Glu Glu Arg Ser
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Asp Ile Asn Asp Asp Arg Ser
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Gly Ser Gly Gly Glu Arg Thr
1 5

<210> 173
<211> 7
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<213> synthetic enterokinase cleavage sequence

<400> 173

Ala Val Ile Gly Asp Arg Ser
1 5

<210> 174
<211> 7
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<213> synthetic enterokinase cleavage sequence

<400> 174

Ser Gly Gly Glu Glu Arg Gly
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<210> 175

<400> 179

Asp Ile Asn Asp Asp 7 Ser
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<210> 180

<211> 7

<212> PRT

<213> synthetic enterokinase cleavage sequence

<400> 180

Asp His Val Trp Asp Arg Ala
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<211> 7

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<213> synthetic enterokinase cleavage sequence

<400> 181

Gly Ser Gly Gly Asp Arg Ile
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<213> synthetic enterokinase cleavage sequence

<400> 182

Ile Glu Asp Glu Asp Arg Ala
1 5

<210> 183

<211> 7

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<213> synthetic enterokinase cleavage sequence

<400> 183

Met Thr Phe Asp Glu Arg Gly
1 5

<210> 184
<211> 7
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<400> 184

Gly Asp Trp Asp Asp Lys Asn
1 5

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Ile Ala Tyr Gln Asp Arg Met
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<213> synthetic enterokinase cleavage sequence

<400> 186

Gly Ser Gly Gly Asp Arg Ile
1 5

<210> 187
<211> 7
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<213> synthetic enterokinase cleavage sequence

<400> 187

Gly Phe Val Gln Glu Arg Met
1 5

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<210> 188
<211> 7
<212> PRT
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<400> 188

Asp Ile Asn Asp Asp Arg Ser
1 5

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Gly Trp Asn Asp Asp Arg Ile
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Gly Gly Phe Glu Asp Arg Leu
1 5

<210> 191
<211> 7
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<213> synthetic enterokinase cleavage sequence

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Gly Ser Gly Gly Asp Arg Asn
1 5

<210> 192
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Ala Ala Val Glu Asp Arg Asn
1 5

<210> 193
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<213> synthetic enterokinase cleavage sequence

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Asp Tyr Arg Leu Asp Arg Ile
1 5

<210> 194
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Gly Asp Asp Asp Asp Lys Ile
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<400> 195

Asp Arg Met Tyr Gln Leu Asp Lys Thr Gly Phe Met Ile
1 5 10

<210> 196
<211> 13
<212> PRT
<213> synthetic enterokinase cleavage sequence

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<400> 196

Ala Val Leu Ser Asn Val Met His Ser Asp Asp Trp Thr
1 5 10

<210> 197

<211> 9

<212> PRT

<213> natural enterokinase cleavage sequence

<400> 197

Gly Asp Asp Asp Asp Lys Ile Tyr Val
1 5

<210> 198

<211> 9

<212> PRT

<213> negative control in EK cleavage experiment

<400> 198

Ala Val Leu Ser Asn Val Met Phe Ile
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<210> 199

<211> 9

<212> PRT

<213> synthetic enterokinase cleavage sequence

<400> 199

Gly Asn Tyr Thr Asp Arg Met Phe Ile
1 5

<210> 200

<211> 9

<212> PRT

<213> synthetic enterokinase cleavage sequence

<400> 200

Asp Ile Asn Asp Asp Arg Ser Leu Phe

TOP SECRET - EYES ONLY

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<210> 201
<211> 9
<212> PRT
<213> synthetic enterokinase cleavage sequence

<400> 201

Asn Lys Ala Lys Asp Arg Met Phe Ile
1 5

<210> 202
<211> 9
<212> PRT
<213> synthetic enterokinase cleavage sequence

<400> 202

Gly Asn Tyr Thr Asp Arg Arg Phe Ile
1 5

<210> 203
<211> 9
<212> PRT
<213> commercial synthetic enterokinase cleavage substrate

<400> 203

Gly Asn Tyr Thr Asp Arg Tyr Phe Ile
1 5

<210> 204
<211> 7
<212> PRT
<213> synthetic enterokinase cleavage sequence

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is any amino acid

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<400> 204

Asp Ile Asn Asp Asp Arg Xaa
1 5

<210> 205

<211> 7

<212> PRT

<213> synthetic enterokinase cleavage sequence

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Xaa is any amino acid

<400> 205

Gly Asn Tyr Thr Asp Arg Xaa
1 5

<210> 206

<211> 7

<212> PRT

<213> synthetic enterokinase cleavage sequence

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa1 is an optional amino acid which, if present, is Ala, Asp, Glu, Phe, Gly, Ile, Asn, Ser, or Val

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa2 is an optional amino acid which, if present, is Ala, Asp, Glu, His, Ile, Leu, Met, Gln, or Ser

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa3 is an optional amino acid which, if present, is Asp, Glu, Phe, His, Ile, Met, Asn, Pro, Val, or Trp

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa4 is Ala, Asp, Glu, or Thr

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa7 is any amino acid

<400> 206

Xaa Xaa Xaa Xaa Asp Arg Xaa
1 5

<210> 207
<211> 7
<212> PRT
<213> synthetic enterokinase cleavage sequence

<220>
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<222> (1)..(1)
<223> Xaa1 is an optional amino acid which, if present, is Asp or Glu

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa2 is an optional amino acid which, if present, is Val

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa3 is an optional amino acid which, if present, is Tyr

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa4 is Asp, Glu or Ser

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<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa7 is any amino acid

<400> 207

Xaa Xaa Xaa Xaa Glu Arg Xaa
1 5

<210> 208
<211> 6
<212> PRT
<213> synthetic enterokinase cleavage sequence

<400> 208

Asp Ile Asn Asp Asp Arg
1 5

<210> 209
<211> 6
<212> PRT
<213> synthetic enterokinase cleavage sequence

<400> 209

Gly Asn Tyr Thr Asp Arg
1 5

<210> 210
<211> 7
<212> PRT
<213> streptavidin binding sequence

<400> 210

Trp His Pro Gln Phe Ser Ser
1 5

100190-20048860

<210> 211
 <211> 10
 <212> PRT
 <213> streptavidin binding sequence

 <400> 211

Pro Cys His Pro Gln Phe Pro Arg Cys Tyr
 1 5 10

<210> 212
 <211> 1272
 <212> DNA
 <213> Bacteriophage M13mp18

<400> 212
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 gacgacaaaaa cttagatcg ttacgctaac tatgagggtt gtctgtggaa tgctacaggc 180
 gttgtagttt gtactggtga cgaaactcag ttttacggta catgggttcc tattgggctt 240
 gctatccctg aaaatgaggg tggtggtctt gagggtggcg gttctgaggg tggcggtct 300
 gagggtggcg gtactaaacc tcctgagttac ggtgatacac ctattccggg ctataacttat 360
 atcaaccctc tcgacggcac ttatccgcct ggtactgagc aaaacccgc taatcctaatt 420
 ctttctcttg aggagtctca gcctttaat actttcatgt ttcagaataa tagttccga 480
 aataggcagg gggcattaac tgtttatacg ggcactgtta ctcaaggcac tgaccccgaa 540
 aaaacttatt accagtacac tcctgtatca tcaaaagcca tgtatgacgc ttactggaac 600
 ggtaaattca gagactgcgc tttccattct ggctttaatg aagatccatt cggttggaa 660
 tatcaaggcc aatcgctctga cctgcctcaa cctcctgtca atgctggcgg cggctctgg 720
 ggtggttctg gtggcggctc tgagggtggt ggctctgagg gtggcggttc tgagggtggc 780
 ggctctgagg gaggcggttc cggtggtggc tctggttccg gtgattttga ttatgaaaag 840
 atggcaaacg ctaataaggg ggctatgacc gaaaatgccg atgaaaacgc gctacagtct 900

gacgctaaag gcaaacttga ttctgtcgct actgattacg gtgctgctat cgatggttc	960
attggtgacg tttccggcct tgctaatggc aatggtgctt ctggtgattt tgctggctct	1020
aattcccaaa tggctcaagt cggtgacggt gataattcac cttaatgaa taattccgt	1080
caatatttac cttccctccc tcaatcggtt gaatgtcgcc cttttgtctt tagcgctggt	1140
aaaccatatg aattttctat tgattgtgac aaaataaaact tattccgtgg tgtcttgcg	1200
tttctttat atgttgccac ctttatgtat gtatttctta cgtttgctaa catactgcgt	1260
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<210> 213

<211> 424

<212> PRT

<213> Bacteriophage M13mp18

<400> 213

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser			
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His Ser Ala Glu Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu		
20	25	30

Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr		
35	40	45

Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys		
50	55	60

Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu			
65	70	75	80

Ala Ile Pro Glu Asn Glu Gly Gly Ser Glu Gly Gly Ser Glu		
85	90	95

Gly Gly Gly Ser Glu Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp	
---	--

100

105

110

Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr
 115 120 125

Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu
 130 135 140

Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg
 145 150 155 160

Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly
 165 170 175

Thr Asp Pro Val Lys Thr Tyr Gln Tyr Thr Pro Val Ser Ser Lys
 180 185 190

Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe
 195 200 205

His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln
 210 215 220

Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Ser Gly
 225 230 235 240

Gly Gly Ser Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Gly
 245 250 255

Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Gly Ser Gly
 260 265 270

Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala
 275 280 285

Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly
 290 295 300

Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe
 305 310 315 320

Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp
 325 330 335

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn
 340 345 350

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
 355 360 365

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu
 370 375 380

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
 385 390 395 400

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala
 405 410 415

Asn Ile Leu Arg Asn Lys Glu Ser
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<210> 214
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 <212> DNA
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<400> 214 60
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 tctcagcctc ttaataacttt catgtttcag aataataggt tccgaaatag gcagggggca 180

ttaactgttt atacgggcac tgttactcaa ggcactgacc ccgttaaaac ttattaccag 240
 tacactcctg tatcatcaaa agccatgtat gacgcttact ggaacggtaa attcagagac 300
 tgcgcttcc attctggctt taatgaagat ccattcggtt gtgaatatca aggccaatcg 360
 tctgacctgc ctcaacctcc tgtcaatgct ggcggcggct ctgggtggc ttctgggtgc 420
 ggctctgagg gtgggtggc tgagggtggc gggtctgagg gtggcggc tc tgagggaggc 480
 ggttccggtg gtggctctgg ttccggtgat tttgattatg aaaagatggc aaacgctaat 540
 aagggggcta tgaccgaaaa tgccgatgaa aacgcgctac agtctgacgc taaaggcaaa 600
 cttgattctg tcgctactga ttacggtgct gctatcgatg gttcattgg tgacgttcc 660
 ggccttgcta atggtaatgg tgctactggt gattttgctg gctctaattc ccaaattggct 720
 caagtcggtg acggtgataa ttcacctta atgaataatt tccgtcaata tttaccttcc 780
 ctccctcaat cggttgaatg tcgccccttt gtcttagcg ctggtaaacc atatgaattt 840
 tctattgatt gtgacaaaat aaacttattc cgtggtgtct ttgcgttct tttatatgtt 900
 gccacctta tgtatgtatt ttctacgtt gctaacatac tgcgtaataa ggagtct 957

<210> 215
 <211> 319
 <212> PRT
 <213> Bacteriophage M13mp18
 <400> 215

Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr Ile
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Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala
 20 25 30

Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met
 35 40 45

Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr
 50 55 60

Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln
 65 70 75 80

Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly
 85 90 95

Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe
 100 105 110

Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val
 115 120 125

Asn Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Gly
 130 135 140

Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly
 145 150 155 160

Gly Ser Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met
 165 170 175

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala
 180 185 190

Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr
 195 200 205

Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn
 210 215 220

Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala
 225 230 235 240

Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln
 245 250 255

Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe
 260 265 270

Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn
 275 280 285

Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met
 290 295 300

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 305 310 315

<210> 216
 <211> 450
 <212> DNA
 <213> Bacteriophage M13mp18

<400> 216
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 gctgctatcg atggtttcat tggtgacggt tccggccttg ctaatggtaa tggtgctact 180
 ggtgattttg ctggctctaa ttcccaaattg gctcaagtgc gtgacgggtga taattcacct 240
 ttaatgaata atttccgtca atatttacct tccctccctc aatcggttga atgtcgccct 300
 tttgtcttta gcgctggtaa accatatgaa ttttctattt attgtgacaa aataaaactta 360
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 tttgctaaca tactgcgtaa taaggagtct 450

<210> 217
 <211> 150
 <212> PRT

<213> Bacteriophage M13mp18

<400> 217

Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr
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Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu
20 25 30

Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly
35 40 45

Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala
50 55 60

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro
65 70 75 80

Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val
85 90 95

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser
100 105 110

Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu
115 120 125

Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile
130 135 140

Leu Arg Asn Lys Glu Ser
145 150